

Residue Identity = 8% Matches = 15 Mismatches = 141
Gaps = 0 Conservative Substitutions = 12

X 10 20
MFOIPEFEPSEQEDSSAERGL
VYVLPGWPODLHMLARNKIRTLKNNMFSEFKKIKSLDQNEKSKIEAFGFLNKLTLLQHNOIKVL
DPDNLSDSLFSGDEENAGTEEIKNBNINGNWISASTINEARINAKRKRURKRNSSSDSGRDSVSDNGSEAVR
20 30 40 50 60 70 80
30 40 50 60 70 80 90
GPSPAGDGPGSGKHKHRQAPGLMDASHQEQPTSSSHHGGAGAVEIRSRHSSYKPGAGTDEGMEGEESPER
SGAVAPTPKGRLDRRSRSRGKGRLPKKGAGGKGWGPQGIVDEEVVKDQPNYDDQENCYETVLP
100 110 120 130 140 150 160
100 110 120 130 140 150 160
GRSRSSAPNLIWAQRYGRELRRMSDEFVDSFKKGIPRKSAGTATOMROSSWTRVFSWMDRNLGRASSAP
160 170 180 190 200 210 220
LDETAFEKLTPIIQTQEVFERGDTNEVAEMRLDNLGENMSGVPLAVSIALEGKASHRENTSKLLSDLCGTV
X
SQ
MSTNDVEKSPDKLKLDPLEALDTPRAPOLVGQFIRAVGDLCTNTKIDSY
X 240 250 260 270 280
4. US-09-894-657-1 (1-168) Sequence 5, Application US/09894657
Initial Score = 12 Optimized Score = 81 Significance = -0.61
Residue Identity = 8% Matches = 14 Mismatches = 144
Gaps = 0 Conservative Substitutions = 10
X 10 20 30 40 50 60
MFOIPEFEPSEQEDSSAERGL
NEQILNVPADPNLSDLSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKRKRURKRNSSSDSGRDS
10 20 30 40 50 60 70
30 40 50 60 70 80 90
GPSPAGDGSGSGKHKHRQAPGLMDASHQEQPTSSSHHGGAGAVEIRSRHSSYKPGAGTDEGMEGEESPER
VSDSGSDALRSLGLDTPSPKGRLDRRSRSRGKGRLPKKGAGGKGWGPQGIVDEEVVKDQPNYDDQ
80 90 100 110 120 130 140
100 110 120 130 140 150 160
GRSRSSAPNLIWAQRYGRELRRMSDEFVDSFKKGIPRKSAGTATOMROSSWTRVFSWMDRNLGRASSAP
150 160 170 180 190 200 210
X
SQ
KLSDLCG3TVMSTTDVEKSPDKLKLDPLEALDTPRAPOLVGQFIRAVGDL
X 230 240 250 260 270
5. US-09-894-657-1 (1-168) Sequence 8, Application US/09894657
Initial Score = 7 Optimized Score = 76 Significance = -0.68
Residue Identity = 9% Matches = 22 Mismatches = 143
Gaps = 74 Conservative Substitutions = 3
X 10 20 30 40 50 60
MFOIPEFEPSEQEDSSAERGLGPSPAGDGPGSGKHKHRQAPGLMDASHQEQPTSSSHHGG
MRYVVTIVILICFCKRAEERKASPGSVRSVNHGRAGGRGGSNPKVRYAFLGPGCDDVYVTLHERKLQDQERKL
10 20 30 40 50 60 70
6. US-09-894-657-1 (1-168) Sequence 3, Application US/09894657
Initial Score = 7 Optimized Score = 76 Significance = -0.68
Residue Identity = 12% Matches = 24 Mismatches = 135
Gaps = 19 Conservative Substitutions = 35
X 10 20 30 40 50 60
MFOIPEFEPSEQEDSSAERGL
MRYVVTIVILCFCKKAELRKASPGSVRSVNHGRAGGRGGSNPKVRYAFLGPGCDDVYVTLHERKLQDQERKL
10 20 30 40 50 60 70
GAV-----EIRSRHSSYKPGAGTDEGMEGEESPERGRRSAPNLIWAQRYGRELRRM
VYVLPGWPODLHMLARNKIRTLKNNMFSEFKKIKSLDQNEKSKIEAFGFLNKLTLLQHNOIKVL
120 130 140 150 160 170 180 190 200 210
SDEFTDFKKGIPRKSAGTATOMROSSWTRVFSWMDRNLGRASSAP
TEEVVKDQPNYDDQ
150 160 170 180 190 200 210
EQLDPKPKQVSGRPVVKPKEVDSIHCNIV
220 230 240
X
SQ
KLSDLCG3TVMSTTDVEKSPDKLKLDPLEALDTPRAPOLVGQFIRAVGDL
X 230 240 250 260 270

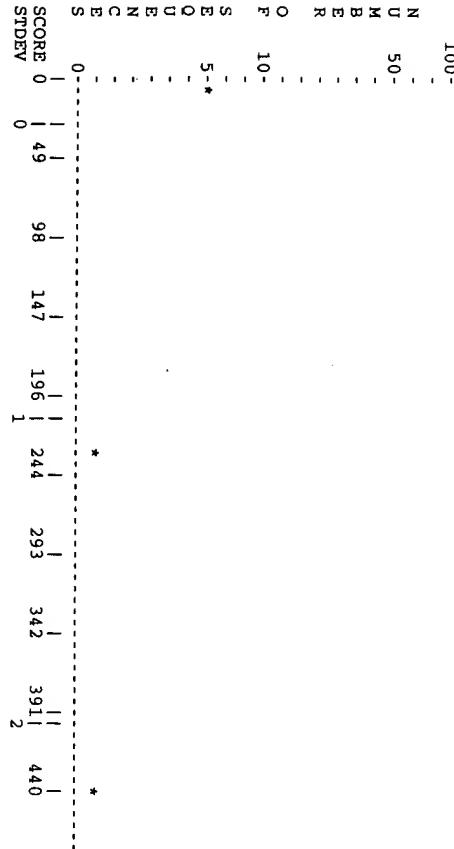
```
> 0 <
> 0 < IntelliGenetics
> 0 <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Query sequence being compared: US-09-894-657-3 (1-440)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-09-894-657-3 (1-440) with:

File : US09894657.pep



PARAMETERS

Similarity matrix PAM-150
Threshold level of sim. 16%
Mismatch penalty 1
Gap penalty 5.00
Gap size penalty 0.05
Cutoff score 1
Randomization group S

SEARCH STATISTICS

Scores: Mean 116 Median 9 Standard Deviation 181.57
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 2027
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
US-09-894-657-3	Sequence 3, Application US	440	440	440	1.78	0

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
US-09-894-657-3	Sequence 3, Application US	440	440	440	1.78	0

The list of other best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
US-09-894-657-8	Sequence 8, Application US	313	229	305	0.62	0
US-09-894-657-9	Sequence 9, Application US	469	8	184	-0.59	0
US-09-894-657-5	Sequence 5, Application US	469	8	185	-0.59	0

1. US-09-894-657-3 (1-440) Sequence 3, Application US/09894657

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
440	440	1.78	100%	0	0
440	440	1.78	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
40	40	0.62	100%	0	0
40	40	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
50	50	0.62	100%	0	0
50	50	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
60	60	0.62	100%	0	0
60	60	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
70	70	0.62	100%	0	0
70	70	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
20	20	0.62	100%	0	0
20	20	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
210	210	0.62	100%	0	0
210	210	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
210	210	0.62	100%	0	0
210	210	0.62	Conservative	Substitutions	

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
280	280	0.62	100%	0	0
280	280	0.62	Conservative	Substitutions	

2. US-09-894-657-3 (1-440)

US-09-894-657-8 Sequence 8, Application US/09894657

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches
305	305	0.62	98%	8	2
307	307	0.62	1	1	3

4. US-09-894-657-3 (1-440) Sequence 5, Application US/09894657

Initial Score = 8 Optimized Score = 185 Significance = -0.59
 Residue Identity = 8% Matches = 38 Mismatches = 379
 Gaps = 13 Conservative substitutions = 23

X 10 20 30 40 50 60 70
 MRVVTIVILCFCKAELRKASPGSVRSVNHGRAGGGRRGSNSPVKRYAFGLPCDVYVTLHEKVLDQCRKL
 10 20 30 40 50 60 70
 PAYPESFDQDTEDEWEKKHRDHTAKKOSVITING
 | ; ; ; ; ; ; ;
 CFAQGTSIKQRLDPLSPSRGRKRFVSGDGGRLKPESY
 | 440 450 X

X 90 100 110 120 130 140 150
 VVVLPGWPODPLHMLLARKNTRKIRTLKNNMSFKKLSLQDQNEISKIESEAFFGLNLKTTLQHNOQKVL
 90 100 110 120 130 140 150
 VVVLPGWPODPLHMLLARKNTRKIRTLKNNMSFKKLSLQDQNEISKIESEAFFGLNLKTTLQHNOQKVL
 90 100 110 120 130 140 150
 TEEFVITYTPLSYLRLYDNPWMCCTEIELTLMQIOPRNRLGNYAKCSPQEQKNNKLQIKBQICN-EE
 100 110 120 130 140 150 160
 TEEFVITYTPLSYLRLYDNPWMCCTEIELTLMQIOPRNRLGNYAKCSPQEQKNNKLQIKBQICN-EE
 100 110 120 130 140 150 160
 KEQQLDPKPOVSGRPVPIKEVDSTFCNYVFPPIQTLDCRKRLKELQVNNIPPDVYKLDLSYUNKIMQLRKEF
 110 120 130 140 150 160 170
 KEQQLDPKPOVSGRPVPIKEVDSTFCNYVFPPIQTLDCRKRLKELQVNNIPPDVYKLDLSYUNKIMQLRKEF
 110 120 130 140 150 160 170
 220 230 240 250 260 270 280
 220 230 240 250 260 270 280
 EDVIRLKKINLSSNGIEFIDPAFLGLTHLEELDLNSNLQNFQDVGVLLEDYFLKLWLRDNPWRCDYH
 290 300 310 X 320 330 340 350
 EDVIRLKKINLSSNGIEFIDPAFLGLTHLEELDLNSNLQNFQDVGVLLEDYFLKLWLRDNPWRCDYH
 290 300 310 X 320 330 340 350
 360 LYY

3. US-09-894-657-3 (1-440) Sequence 9, Application US/09894657

Initial Score = 8 Optimized Score = 184 Significance = -0.59
 Residue Identity = 8% Matches = 37 Mismatches = 379
 Gaps = 13 Conservative Substitutions = 24

X 10 20 30 40 50 60 70
 MRVVTIVILCFCKAELRKASPGSVRSVNHGRAGGGRRGSNSPVKRYAFGLPCDVY
 10 20 30 40 50 60 70
 MDIENEQTLANNPDTDNLSDLSFSDENAGTEKNEINGWISASTINEARINAKRRLRNNSRSG
 10 20 30 40 50 60 70
 TYLHRYKLCOERKLYVVLPGWPOD-LHMLLARKNTRKIRTLKNNMSFKKLSLQDQNEISKIESEA---
 60 70 80 90 100 110 120
 RGDSDVSDNGSEAVRSVGVAVPSPKGRLDRRSRSRGKGRGPKGGGGKGVWGTPOQVYDVEEVDKWDPNID
 90 100 110 120 130 140 150
 10 20 30 40 50 60 70
 VPPNIPPDIVKLDSYUNKINOLRKEFEDVHLLKLNLSSNGIEFIDPAFLGLTHLEELDLNSNLQNFQD
 190 200 210 220 230 240 250
 YAKCESPOEQKNNKLQIKSEBQNEEKEQQLDPKPOVSGRPVPIKEVDSTFCNYVFPPIQTLDCRKRLK
 220 230 240 250 260 270 280
 EMTSKLLSDLCCTVMSTTDVEFSFDKLKDLFELLADTPRAPOLVGQFARAVGDGILCNTIDSYKGTVD
 270 280 290 300 310 320 330
 VPPNIPPDIVKLDSYUNKINOLRKEFEDVHLLKLNLSSNGIEFIDPAFLGLTHLEELDLNSNLQNFQD
 290 300 310 320 330 340 350
 VYDQENQVYETVVLPLDRAFEKTLTPIQEFEGDTNEVAEMLRDNLGENKSGVPLAVSLALEKASHR
 370 380 390 400 410 420 430
 130 140 150 160 170 180 190
 FFGFLNKLUTLHNOIKVLTTEEVFVITYTPLSYLRLYDNPWMCCTEIELTLMQIOPRNRLG
 150 160 170 180 190 200 210
 DDQENQVYETVVLPLDRAFEKTLTPIQEFEGDTNEVAEMLRDNLGENKSGVPLAVSLALEKASHR
 220 230 240 250 260 270 280
 EMTSKLLSDLCCTVMSTTDVEFSFDKLKDLFELLADTPRAPOLVGQFARAVGDGILCNTIDSYKGTVD
 270 280 290 300 310 320 330
 130 140 150 160 170 180 190
 YAKCESPOEQKNNKLQIKSEBQNEEKEQQLDPKPOVSGRPVPIKEVDSTFCNYVFPPIQTLDCRKRLK
 190 200 210 220 230 240 250
 HELVYEATIMVLESTGSESTKMLDLKSLWKSSTITDQMKRGYERYINEIDPDINLDVPHSYSLVERVE
 220 230 240 250 260 270 280
 270 280 290 300 310 320 330
 VPPNIPPDIVKLDSYUNKINOLRKEFEDVHLLKLNLSSNGIEFIDPAFLGLTHLEELDLNSNLQNFQD
 290 300 310 320 330 340 350
 VQARAALDKATVLLMSKGGKRSVWGGQQQPVNHLVKEIDMLLKEYLISGDISEAHLKELEVPHF
 340 350 360 370 380 390 400
 GVLEDLYFKLWLRLRNPWRCDYHLYWMLKHHNVNGLECKPEEYKGWSVGVKVTRSYEECPKDKL
 370 380 390 400 410 420 430
 HELVYEATIMVLESTGSESTKMLDLKSLWKSSTITDQMKRGYERYINEIDPDINLDVPHSYSLVERVE
 380 390 400 410 420 430 440